AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1.-18. (Canceled)

19. (Currently Amended) A method of identifying a compound that binds to a human target RNA comprising:

generating *in silico* a virtual library of compounds predicted or calculated to interact with a molecular interaction site within said human target RNA;

comparing *in silico* three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing the highly ranked members of said hierarchy of compounds; and

testing said highly ranked members to determine their ability to interact with said molecular interaction site by:

contacting the human target RNA with at least one of said highly ranked members to provide a complex between the human target RNA and the member or members;

ionizing said complex;

fragmenting the ionized complex; and

determining whether highly ranked members bind to the molecular interaction site of said human target RNA.

20. (Previously Presented) The method of claim 19 further comprising determining the strength of binding of a highly ranked member in comparison to the binding strength of other highly ranked members.

21.-25. (Canceled)

26. (Currently Amended) A method of identifying a compound that binds to a human target RNA comprising:

identifying *in silico* at least one molecular interaction site on said human target RNA[[:]] by comparing the nucleotide sequence of said human target RNA with the nucleotide sequence of a RNA from a different taxonomic species[[;]], identifying at least one conserved region, and determining the secondary structure of said conserved region;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing *in silico* three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing the highly ranked members of said heirarchy of compounds;

testing said highly ranked members to determine their ability to interact with said molecular interaction site;

contacting said human target RNA with at least one of said highly ranked members to provide a complex between said human target RNA and the member or members;

ionizing said complex;

fragmenting the ionized complex; and

determining whether highly ranked members binds to the molecular interaction site of said human target RNA.

27.-29. (Canceled)

30. (Previously Presented) The method of claim 29 further comprising determining the strength of binding of a highly ranked member in comparison to the binding strength of other highly ranked members.

31. (Canceled)

32. (Currently Amended) A method of identifying a compound that binds to a human target RNA comprising:

identifying at least one molecular interaction site on said human target RNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing *in silico* three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing said highly ranked members of said hierarchy of compounds;

contacting said human target RNA with at least one of said highly ranked members to provide a complex between said human target RNA and said member or members;

ionizing said complex;

fragmenting said ionized complex; and

determining whether highly ranked member or members bind to said molecular interaction site of said human target RNA.

33. (Previously Presented) The method of claim 32 further comprising determining the strength of binding of at least one highly ranked member in comparison to the binding strength of other highly ranked members.

34. (Currently Amended) A method of identifying a compound that binds to a human target RNA comprising:

identifying at least one molecular interaction site on said human target RNA, wherein said human target RNA comprises single-stranded RNA and is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing *in silico* three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing the highly ranked members of said hierarchy of compounds;

contacting said human target RNA with at least one of said highly ranked members to provide a complex between said human target RNA and the member or members;

ionizing said complex;

fragmenting said ionized complex; and

determining whether highly ranked member or members binds to said molecular interaction site of said human target RNA.

35. (Previously Presented) The method of claim 34 further comprising determining the strength of binding of at least one highly ranked member in comparison to the binding strength of other highly ranked members.

36. (New) The method of claim 19, wherein said molecular interaction site is less than 30 nucleotides in length.

37. (New) The method of claim 19, wherein said molecular interaction site comprises a secondary structure selected from a bulge, a loop, a stem, a hairpin, or a mismatch basepair.

38. (New) The method of claim 37, wherein said secondary structure is located within an untranslated region of said human target RNA.

39. (New) The method of claim 26, wherein said molecular interaction site is less than 30 nucleotides in length.

40. (New) The method of claim 26, wherein said said molecular interaction site comprises a secondary structure selected from a bulge, a loop, a stem, a hairpin, or a mismatch basepair.

41. (New) The method of claim 40, wherein said secondary structure is located in an untranslated region of said human target RNA.

42. (New) The method of claim 32, wherein said molecular interaction site is less than 30 nucleotides in length.

43. (New) The method of claim 32, wherein said molecular interaction site comprises a secondary structure selected from a bulge, a loop, a stem, a hairpin, or a mismatch basepair.

44. (New) The method of claim 43, wherein said secondary structure is located in an untranslated region of said human target RNA.

45. (New) The method of claim 34, wherein said molecular interaction site is less than 30 nucleotides in length.

46. (New) The method of claim 34, wherein said molecular interaction site comprises a secondary structure selected from a bulge, a loop, a stem, a hairpin, or a mismatch basepair.

47. (New) The method of claim 46, wherein said secondary structure is located in an untranslated region of said human target RNA.